

The following Listing of the Claims will replace all prior versions and all prior listings of the claims in the present application:

Listing of the Claims:

1. (Currently amended) A method of using a computer system to identify a determine the presence of a microbe inhabiting a host organism, comprising the steps of:
 - a) obtaining sequence information from a plurality of sequences from at least one a host organism; and
 - b) searching a database of host organism genomic sequences to determine the presence or absence of said plurality of sequences in said database, wherein the absence of at least one of said sequences in said database indicates that said at least one sequence is a candidate sequence belonging to a microbe, thereby indicating the presence of a microbe inhabiting said host organism.
2. (Currently amended) A method of using a computer system to identify a determine the presence of a microbe inhabiting a host organism, comprising the steps of:
 - a) obtaining sequence information from a library of genomic DNA from a host organism suspected of harboring a microbe; and
 - b) searching a database of host organism genomic sequences from host organisms which do not harbor the microbe to determine the presence or absence of a sequence in said library in said database; wherein the absence of said sequence indicates that said sequence is a candidate microbe sequence, thereby indicating the presence of a microbe inhabiting said host organism.
3. (Currently amended) A method of using a computer system to identify a determine the presence of a microbe inhabiting a host organism, comprising the steps of:

- a) obtaining sequence information from a plurality of expressed sequences from ~~at least one a~~ host organism; and
 - b) searching a database of host organism genomic sequences to determine the presence or absence of said plurality of expressed sequences in said database, wherein the absence of at least one of said expressed sequences in said database indicates that said at least one sequence is a candidate sequence belonging to a microbe, thereby indicating the presence of a microbe inhabiting said host organism.
4. (Currently Amended) The method according to claims 1, 2, or 3, wherein said candidate sequence belongs to a symbiotic microbial organism ~~microbe is a symbiotic organism.~~
5. (Currently Amended) The method according to claim 4, wherein said candidate sequence belongs to microbe is a mutualistic organism, a commensal organism, or a parasitic organism.
6. (Currently Amended) The method according to claim 1, 2, or 3, wherein said candidate sequence belongs to microbe is a pathogenic organism.
7. (Original) The method according claims 1, 2, 3, wherein said plurality of sequences are compared to said database of host genomic sequences simultaneously.
8. (Previously Amended) The method of claims 1, 2, or 3 wherein said microbe inhabiting a host organism is an intracellular pathogen, wherein said host organism in step (a) has a pathogenic condition, and wherein said database of host organism genomic sequences in step (b) comprises genomic sequences of a plurality of host organisms not having said pathogenic condition.
9. (Currently Amended) The method according to claim 8, wherein said identified plurality of sequences are compared simultaneously with sequences in said database of host genomic sequences.
10. (Currently Amended) The method according to claim 1 or 8, wherein said sequences of said plurality of sequences are expressed sequences.

11. (Currently Amended) The method according to claim 3 or claim 10, 1, 3, or 8, wherein said expressed sequences are EST sequences.
12. (Currently Amended) The method according to claim 3 or claim 10, 1, 3, or 8, wherein said expressed sequences are cDNA sequences.
13. (Currently Amended) The method according to claim 1, 2, or 3 3, or 8, wherein said host organism is an animal.
14. (Original) The method according to claim 13, wherein said animal is a mammal.
15. (Original) The method according to claim 14, wherein said mammal is a human.
16. (Original) The method according to claim 13, wherein said animal is an insect, bird, or a fish.
17. (Currently Amended) The method according to claim 1, 2, or 3 3, or 8, wherein said host organism is a microorganism, a fungus, or a plant.
18. (Original) The method according to claim 11, wherein said candidate sequence is identified by comparing sequences in a database of expressed sequences with said sequences in said genomic database.
19. (Currently Amended) The method according to claim 3 or claim 10 8, wherein said expressed sequence sequences is are identified using a differential gene expression assay.
20. (Original) The method according to claim 19, wherein said differential gene expression assay is selected from the group consisting of SAGE, cDNA representational difference analysis, and suppression subtraction analysis.
21. (Currently Amended) The method according to claim 3 or claim 10 8, wherein said candidate at least one sequence is identified using a subtractive hybridization method.
22. (Original) The method according to claim 21, wherein said subtractive hybridization method is representational difference analysis.

23. (Currently Amended) The method according to claim 1, 2, or 3 ~~3, or 8~~, wherein said candidate sequence is used as a query sequence to search a database of microbial sequences.
24. (Original) The method according to claim 23, wherein said microbial sequences include viral sequences.
25. (Currently Amended) The method according to claim 1, 2, or 3 ~~3, or 8~~, wherein any of: vector sequences, repetitive sequences, mitochondrial sequences, non-host species sequences, known host organism sequences, and combinations thereof are eliminated from the genomic database comprising sequences from the host organism.
26. (Currently Amended) The method according to claim 1, 2, or 3 ~~3, or 8~~, wherein said searching is performed iteratively using progressively smaller word sizes.
27. (Canceled)
28. (Canceled)
29. (Currently Amended) The method according to claim 6~~or 8~~, wherein said pathogen is an infectious disease organism.
30. (Currently Amended) The method according to claim 6~~or 8~~, wherein said pathogen is associated with a pathogenic condition selected from the group consisting of an inflammatory disease, an autoimmune disease, and a cell proliferative disease.
31. (Original) The method according to claim 30, wherein said disease is selected from the group consisting of sarcoidosis, inflammatory bowel disease, atherosclerosis, multiple sclerosis, rheumatoid arthritis, type I diabetes mellitus, lupus erythematosus, Hodgkin's disease, and bronchioalveolar carcinoma.
32. (Canceled)
33. (Canceled)
34. (Canceled)

35. (Canceled)

36. (Canceled)

37. (Canceled)

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39. (Canceled)

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48. (Canceled)

49. (Canceled)

50. (Currently amended) A method of using a computer system to identify a determine the presence of a microbe inhabiting a host organism, comprising the steps of:

obtaining sequence information from a plurality of expressed sequences from ~~at least one~~ a host organism; and

searching a database of host organism genomic sequences to determine the presence or absence of the plurality of expressed sequences in the database, wherein the absence of an expressed sequence in the database identifies the

expressed sequence as a candidate microbe sequence, thereby indicating the presence of a microbe inhabiting said host organism..

51. (Original) The method according to claim 50, wherein said plurality of sequences are from a library of sequences.
52. (Cancelled herein)
53. (Original) The method according to claim 51 or 52, wherein said library comprises human sequences.
54. (Original) The method according to claim 53, wherein said library comprises human sequences from one or more humans having a pathological condition.
55. (Original) The method according to claim 54, wherein said pathological condition is a disease selected from the group consisting of an inflammatory disease, an autoimmune disease, and a cell proliferative disease.
56. (Original) The method according to claim 55, wherein said disease is selected from the group consisting of sarcoidosis, inflammatory bowel disease, atherosclerosis, multiple sclerosis, rheumatoid arthritis, type I diabetes mellitus, lupus erythematosus, Hodgkin's disease, and bronchioalveolar carcinoma.
57. (Original) The method according to claim 50, wherein said step of obtaining sequence information comprises sequencing expressed sequences cloned in a library of expressed sequences.
58. (Currently amended) A method of using a computer system to identify a determine the presence of a microbe inhabiting a host organism, comprising the steps of:
obtaining expressed sequence information from a plurality of sequences from at least one non-microbial host organism; and
searching a database of microbial sequences from a library of expressed sequences to determine the presence or absence of the said plurality of expressed sequences from at least one non-microbial host organism in the database, wherein

the presence of an expressed sequence from said at least one non-microbial host organism in the database identifies the expressed sequence as a candidate microbe sequence, thereby indicating the presence of a microbe inhabiting said host organism.

59. (Cancelled herein)
60. (Original) The method according to claim 58, wherein said library of expressed sequences comprises sequences from one or more humans having a pathological condition.
61. (Original) The method according to claim 60, wherein said pathological condition is an infectious disease.
62. (New) The method according to claim 8, wherein said pathogen is an infectious disease organism.
63. (New) The method according to claim 8, wherein said pathogen is associated with a pathogenic condition selected from the group consisting of an inflammatory disease, an autoimmune disease, and a cell proliferative disease.
64. (New) The method according to claim 63, wherein said disease is selected from the group consisting of sarcoidosis, inflammatory bowel disease, atherosclerosis, multiple sclerosis, rheumatoid arthritis, type I diabetes mellitus, lupus erythematosus, Hodgkin's disease, and bronchioalveolar carcinoma.